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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/826,909

DATE: 05/13/2002

TIME: 08:45:47

#11

Input Set : A:\205551US0X.txt

Output Set: N:\CRF3\05102002\I826909.raw

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3 <110> APPLICANT: MOECKEL, BETTINA
4     FARWICK, MIKE
5     HERMANN, THOMAS
6     KREUTZER, CAROLINE
7     PFEFFERLE, WALTER
9 <120> TITLE OF INVENTION: NUCLEOTIDE SEQUENCES FOR ENCODING OF THE LYSR2-GENE
11 <130> FILE REFERENCE: 205551US0X
13 <140> CURRENT APPLICATION NUMBER: 09/826,909
C--> 14 <141> CURRENT FILING DATE: 2002-05-01
16 <150> PRIOR APPLICATION NUMBER: DE 100 39 047.1
17 <151> PRIOR FILING DATE: 2000-08-10
19 <150> PRIOR APPLICATION NUMBER: DE 100 10 346.8
20 <151> PRIOR FILING DATE: 2001-03-03
22 <160> NUMBER OF SEQ ID NOS: 5
24 <170> SOFTWARE: PatentIn version 3.1
26 <210> SEQ ID NO: 1
27 <211> LENGTH: 1364
28 <212> TYPE: DNA
29 <213> ORGANISM: Corynebacterium glutamicum
31 <220> FEATURE:
32 <221> NAME/KEY: CDS
33 <222> LOCATION: (232)..(1161)
34 <223> OTHER INFORMATION:
37 <400> SEQUENCE: 1
38 cctgcgtgca ataaagacca ttgaaagcag caagaccggc ggccagcadc gcaaacacag      60
40 cgcgcttgta attgcgtgtt cctcgctcga tgccttcgtg gccttcgtgg ccttcgtgtg      120
42 cctcgacctt gctatctatt gcttggtcca tggagttcat catgcgcaa cagcaaatat      180
44 tagtaaaatg ttagaaatag ctgtttttga ttcactttgt gcatgtaggc t gtg acc      237
45                                     Val Thr
46                                     1
48 atg ggc aac gac ggc gga gac ctg cga atc gac gac cta cgc agc ttc      285
49 Met Gly Asn Asp Gly Gly Asp Leu Arg Ile Asp Asp Leu Arg Ser Phe
50      5                                10                                15
52 att tca gtc gct caa tca ggc cac ctc acc gaa act gcc gaa aga tta      333
53 Ile Ser Val Ala Gln Ser Gly His Leu Thr Glu Thr Ala Glu Arg Leu
54      20                                25                                30
56 ggc atc ccg cag ccc aca ctt tcc aga cga atc agc cga gtg gaa aaa      381
57 Gly Ile Pro Gln Pro Thr Leu Ser Arg Arg Ile Ser Arg Val Glu Lys
58      35                                40                                45                                50
60 cac gca ggc acc cca ctt ttc gac cgc gcc ggc cgc aaa ctc gtc ctc      429
61 His Ala Gly Thr Pro Leu Phe Asp Arg Ala Gly Arg Lys Leu Val Leu
62      55                                60                                65
64 aac caa cga ggc cac gcc ttc ctc aac cac gcc agc gcc atc gtc gca      477

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65	Asn	Gln	Arg	Gly	His	Ala	Phe	Leu	Asn	His	Ala	Ser	Ala	Ile	Val	Ala	
66				70				75						80			
68	gaa	ttc	aac	tcc	gcc	gca	act	gaa	atc	aaa	cgc	ctc	atg	gac	cca	gaa	525
69	Glu	Phe	Asn	Ser	Ala	Ala	Thr	Glu	Ile	Lys	Arg	Leu	Met	Asp	Pro	Glu	
70			85					90						95			
72	aaa	ggc	aca	atc	cga	ctg	gac	ttc	atg	cat	tcc	ttg	ggc	act	tg	atg	573
73	Lys	Gly	Thr	Ile	Arg	Leu	Asp	Phe	Met	His	Ser	Leu	Gly	Thr	Trp	Met	
74		100					105					110					
76	gtc	ccc	gaa	ctt	atc	cga	aca	ttc	cgc	gcc	gaa	cac	ccc	aac	gta	gaa	621
77	Val	Pro	Glu	Leu	Ile	Arg	Thr	Phe	Arg	Ala	Glu	His	Pro	Asn	Val	Glu	
78	115					120					125				130		
80	ttc	caa	ctc	cac	caa	gcg	gca	gca	atg	ctc	ctg	gta	gat	cgt	gtt	ttg	669
81	Phe	Gln	Leu	His	Gln	Ala	Ala	Ala	Met	Leu	Leu	Val	Asp	Arg	Val	Leu	
82				135					140					145			
84	gct	gat	gaa	act	gac	ctc	gca	tta	gtt	ggc	ccc	aaa	cct	gcc	gag	gtt	717
85	Ala	Asp	Glu	Thr	Asp	Leu	Ala	Leu	Val	Gly	Pro	Lys	Pro	Ala	Glu	Val	
86			150					155					160				
88	ggt	acc	tct	tta	ggg	tg	gcg	cca	ctg	ctt	cgt	caa	cga	ctt	gcc	cta	765
89	Gly	Thr	Ser	Leu	Gly	Trp	Ala	Pro	Leu	Leu	Arg	Gln	Arg	Leu	Ala	Leu	
90			165				170						175				
92	gct	gtt	ccc	gca	gat	cac	cgg	ctt	gcc	tcc	ttt	tct	ggc	caa	gga	gaa	813
93	Ala	Val	Pro	Ala	Asp	His	Arg	Leu	Ala	Ser	Phe	Ser	Gly	Gln	Gly	Glu	
94		180				185					190						
96	ttg	ccg	ttg	att	act	gcg	gcg	gaa	gaa	cct	ttc	gtg	gcg	atg	cga	gca	861
97	Leu	Pro	Leu	Ile	Thr	Ala	Ala	Glu	Glu	Pro	Phe	Val	Ala	Met	Arg	Ala	
98	195				200				205					210			
100	ggt	ttc	ggc	acc	cga	ctc	ctc	atg	gat	gca	tta	gcc	gaa	gaa	gcc	ggt	909
101	Gly	Phe	Gly	Thr	Arg	Leu	Leu	Met	Asp	Ala	Leu	Ala	Glu	Glu	Ala	Gly	
102				215					220					225			
104	ttt	gtt	ccc	aat	gtg	gtt	ttc	gaa	tcc	atg	gaa	ctc	acc	acc	gtc	gca	957
105	Phe	Val	Pro	Asn	Val	Val	Phe	Glu	Ser	Met	Glu	Leu	Thr	Thr	Val	Ala	
106			230					235					240				
108	ggg	ctt	gtc	agc	gca	ggt	ctc	ggc	gtt	ggt	gtg	gtt	ccg	atg	gat	gat	1005
109	Gly	Leu	Val	Ser	Ala	Gly	Leu	Gly	Val	Gly	Val	Val	Pro	Met	Asp	Asp	
110			245				250						255				
112	ccg	tac	ctt	ccc	aca	gtg	gga	atc	gtg	caa	cgc	cca	ctt	agt	cca	ccc	1053
113	Pro	Tyr	Leu	Pro	Thr	Val	Gly	Ile	Val	Gln	Arg	Pro	Leu	Ser	Pro	Pro	
114		260				265						270					
116	gct	tat	agg	gaa	cta	ggt	ttg	gtg	tg	cga	ctc	aac	gcg	ggg	ccg	gca	1101
117	Ala	Tyr	Arg	Glu	Leu	Gly	Leu	Val	Trp	Arg	Leu	Asn	Ala	Gly	Pro	Ala	
118	275				280				285					290			
120	cct	gcg	gtg	gat	aac	ttc	cgg	aag	ttc	gtg	gcg	gga	tcg	agg	tat	gca	1149
121	Pro	Ala	Val	Asp	Asn	Phe	Arg	Lys	Phe	Val	Ala	Gly	Ser	Arg	Tyr	Ala	
122				295				300					305				
124	tta	gaa	gag	ggc	tgagctgtaa	gtgtcgtggg	tgccgtttta	aggggttgag									1201
125	Leu	Glu	Glu	Gly													
126				310													
128	ttttcccgat	gactaggagt	tggtccagat	tggtgcgttag	gggcccctag	gggcgattct											1261
130	ggggctggtg	tttttgtggc	catgggggtt	ggtgttaatc	ctggaggctt	gctgcaagat											1321

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132 tgctgttaaa cttctcgtca cggatcgctt gggaagcctg gaa 1364
135 <210> SEQ ID NO: 2
136 <211> LENGTH: 310
137 <212> TYPE: PRT
138 <213> ORGANISM: Corynebacterium glutamicum
140 <400> SEQUENCE: 2
142 Val Thr Met Gly Asn Asp Gly Gly Asp Leu Arg Ile Asp Asp Leu Arg
143 1 5 10 15
146 Ser Phe Ile Ser Val Ala Gln Ser Gly His Leu Thr Glu Thr Ala Glu
147 20 25 30
150 Arg Leu Gly Ile Pro Gln Pro Thr Leu Ser Arg Arg Ile Ser Arg Val
151 35 40 45
154 Glu Lys His Ala Gly Thr Pro Leu Phe Asp Arg Ala Gly Arg Lys Leu
155 50 55 60
158 Val Leu Asn Gln Arg Gly His Ala Phe Leu Asn His Ala Ser Ala Ile
159 65 70 75 80
162 Val Ala Glu Phe Asn Ser Ala Ala Thr Glu Ile Lys Arg Leu Met Asp
163 85 90 95
166 Pro Glu Lys Gly Thr Ile Arg Leu Asp Phe Met His Ser Leu Gly Thr
167 100 105 110
170 Trp Met Val Pro Glu Leu Ile Arg Thr Phe Arg Ala Glu His Pro Asn
171 115 120 125
174 Val Glu Phe Gln Leu His Gln Ala Ala Met Leu Leu Val Asp Arg
175 130 135 140
178 Val Leu Ala Asp Glu Thr Asp Leu Ala Leu Val Gly Pro Lys Pro Ala
179 145 150 155 160
182 Glu Val Gly Thr Ser Leu Gly Trp Ala Pro Leu Leu Arg Gln Arg Leu
183 165 170 175
186 Ala Leu Ala Val Pro Ala Asp His Arg Leu Ala Ser Phe Ser Gly Gln
187 180 185 190
190 Gly Glu Leu Pro Leu Ile Thr Ala Ala Glu Glu Pro Phe Val Ala Met
191 195 200 205
194 Arg Ala Gly Phe Gly Thr Arg Leu Leu Met Asp Ala Leu Ala Glu Glu
195 210 215 220
198 Ala Gly Phe Val Pro Asn Val Val Phe Glu Ser Met Glu Leu Thr Thr
199 225 230 235 240
202 Val Ala Gly Leu Val Ser Ala Gly Leu Gly Val Gly Val Val Pro Met
203 245 250 255
206 Asp Asp Pro Tyr Leu Pro Thr Val Gly Ile Val Gln Arg Pro Leu Ser
207 260 265 270
210 Pro Pro Ala Tyr Arg Glu Leu Gly Leu Val Trp Arg Leu Asn Ala Gly
211 275 280 285
214 Pro Ala Pro Ala Val Asp Asn Phe Arg Lys Phe Val Ala Gly Ser Arg
215 290 295 300
218 Tyr Ala Leu Glu Glu Gly
219 305 310
222 <210> SEQ ID NO: 3
223 <211> LENGTH: 439
224 <212> TYPE: DNA

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225 <213> ORGANISM: Corynebacterium glutamicum
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232 tccgaacatt ccgcgcgcaa caccccaacg tagaattcca actccaccaa gcggcagcaa      180
234 tgctcctggt agatcgtggt ttggctgatg aaactgacct cgcattagtt ggccccaac      240
236 ctgccgaggt tggtagctct ttaggggtgg cgccactgct tegtcaacga cttgccctag      300
238 ctgttcccgc agatcacccg cttgcctcct tttctggcca aggagaattg ccgttgatta      360
240 ctgcggcgga agaacctttc gtggcgatgc gaggaggttt cggcaccgca ctctcatgg      420
242 atgcattagc cgaagaagc                                     439
245 <210> SEQ ID NO: 4
246 <211> LENGTH: 20
247 <212> TYPE: DNA
248 <213> ORGANISM: Corynebacterium glutamicum
250 <400> SEQUENCE: 4
251 ccatcgctcgc agaattcaac                                     20
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255 <211> LENGTH: 20
256 <212> TYPE: DNA
257 <213> ORGANISM: Corynebacterium glutamicum
259 <400> SEQUENCE: 5
260 gcttcttcgg ctaatgcac                                     20

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VERIFICATION SUMMARY

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Input Set : A:\205551US0X.txt

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L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date